1.7

GENETIC DIVERSITY AND POPULATION STRUCTURE OF A LARGE COLLECTIONE OF *Magnaporthe oryzae* ISOLATES FROM ITALIAN RICE FIELD

CRISPINO L.*, RODOLFI M.**, PICCO A.**, ODILE FAIVRE-RAMPANT*'*** THARREAU D.***, LUPOTTO E.****, PIFFANELLI P. * , ABBRUSCATO P.*

*) FPTP, Centro di Ricerche e Studi Agroalimentari, Lodi (Italy)
**) UNIPV, Dipartimento di Scienze della Terra e dell'Ambiente, Pavia (Italy)
***) CIRAD, UMR BGPI, Montpellier (France)
****) CRA- Dipartimento di Biologia e Produzione Vegetale, Roma (Italy)

Magnaporthe oryzae, biodiversity, SSR, Italian isolates

Blast, caused by the filamentous ascomycete fungus *Magnaporthe oryzae*, is the most severe disease of rice worldwide, causing yield loss to rice cultivation up to 50-70%. To investigate rice-*Magnaporthe* interaction is crucial to understand the molecular mechanisms underlying durable blast resistance and establish improved rice protection strategies. However, durable resistance is a difficult task to achieve due to the high degree of pathogenic variability of host populations and large number of fungal races co-existing.. The study of the genetic diversity and definition of the structure of existing populations are necessary to overcome this hurdle and identify new virulent genotypes. Therefore, the development of robust and reliable molecular markers allowing to monitor the dynamics of *Magnaporthe* populations is a crucial goal to design strategies for rice blast control. During the last 20 years, the diversity and structure of *M. oryzae* populations on rice were described using different molecular techniques such as RFLP, rep-PCR markers, RAPD or AFLP. Simple Sequence Repeat (SSR) has become the most popular marker system used in genetic mapping, diversity studies and pedigree analysis, since are highly informative and highly reproducible. SSR have been only recently developed to analyze *Magnaporthe* genetic diversity, but studies have been carried out only at European or worldwide scale. The main goal of this study was to investigate the genetic diversity of Italian *Magnaporthe oryzae* strains to implement national rice breeding program for durable resistance towards blast population inhabiting Italian ricegrowing areas. To this aim, in the framework of the RISINNOVA project we created a large *Magnaporthe* collection constituted of 293 Italian strains isolated in the period 1998-2011, different locations in Italy and plant organs. To classify the biodiversity of RISINNOVA *Magnaporthe* collection a molecular characterization was carried out by a set of selected informative SSR and preliminary results of the phylogenetic analyses will be presented.

Research activities were supported by Progetto AGER, grant n° 2010-2369